

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/677,956 C  
Source: TFW16  
Date Processed by STIC: 10/12/2006

***ENTERED***



IFW16

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/677,956C

DATE: 10/12/2006  
 TIME: 08:05:25

Input Set : F:\16988.ST25.txt  
 Output Set: N:\CRF4\10122006\J677956C.raw

5 <110> APPLICANT: Zebedee, Suzanne  
 6       Inchauspe, Genevieve  
 7       Nasoff, Marc S.  
 8       Prince, Alfred M.  
 10 <120> TITLE OF INVENTION: METHODS AND SYSTEMS FOR PRODUCING RECOMBINANT VIRAL ANTIGENS  
 12 <130> FILE REFERENCE: 323-100USD  
 14 <140> CURRENT APPLICATION NUMBER: 10/677,956C  
 15 <141> CURRENT FILING DATE: 2003-10-01  
 17 <150> PRIOR APPLICATION NUMBER: 08/931,855  
 18 <151> PRIOR FILING DATE: 1997-09-16  
 20 <150> PRIOR APPLICATION NUMBER: 08/563,733  
 21 <151> PRIOR FILING DATE: 1995-11-08  
 23 <150> PRIOR APPLICATION NUMBER: 08/272,271  
 24 <151> PRIOR FILING DATE: 1994-07-08  
 26 <150> PRIOR APPLICATION NUMBER: 07/616,369  
 27 <151> PRIOR FILING DATE: 1990-11-21  
 29 <150> PRIOR APPLICATION NUMBER: 07/573,643  
 30 <151> PRIOR FILING DATE: 1990-08-27  
 32 <160> NUMBER OF SEQ ID NOS: 76  
 34 <170> SOFTWARE: PatentIn version 3.3  
 36 <210> SEQ ID NO: 1  
 37 <211> LENGTH: 795  
 38 <212> TYPE: DNA  
 39 <213> ORGANISM: Human immunodeficiency virus  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: CDS  
 44 <222> LOCATION: (16)..(789)  
 46 <400> SEQUENCE: 1  
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 48                   Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val  
 49                   1               5                   10  
 51 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta       99  
 52 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
 53                   15           20                   25  
 55 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta   147  
 56 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
 57                   30           35                   40  
 59 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg   195  
 60 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
 61 45               50           55                   60  
 63 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag   243  
 64 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
 65               65           70                   75

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68 Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile	
69 80 85 90	
71 gca cca ggc cag atg aga gaa cca agg gga agt gac ata gca gga act	339
72 Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr	
73 95 100 105	
75 act agt acc ctt cag gaa caa ata gga tgg atg aca aat aat cca cct	387
76 Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro	
77 110 115 120	
79 atc cca gta gga gaa att tat aaa aga tgg ata atc ctg gga tta aat	435
80 Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn	
81 125 130 135 140	
83 aaa ata gta aga atg tat agc cct acc agc att ctg gac ata aga caa	483
84 Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln	
85 145 150 155	
87 gga cca aag gaa ccc ttt aga gac tat gta gac cgg ttc tat aaa act	531
88 Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr	
89 160 165 170	
91 cta aga gcc gag caa gct tca cag gag gta aaa aat tgg atg aca gaa	579
92 Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu	
93 175 180 185	
95 acc ttg ttg gtc caa aat gcg aac cca gat tgt aag act att tta aaa	627
96 Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys	
97 190 195 200	
99 gca ttg gga cca gcg gct aca cta gaa atg atg aca gca tgt cag	675
100 Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln	
101 205 210 215 220	
103 gga gta gga gga ccc aaa aat caa caa tta tta tcc tta tgg ggg tgt	723
104 Gly Val Gly Gly Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys	
105 225 230 235	
107 aaa ggg aaa ctt gtt tgt tat act tcc gtt aaa tgg aat gga ccc ggc	771
108 Lys Gly Lys Leu Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly	
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111 cat aag gca aga gtt ttg taataa	795
112 His Lys Ala Arg Val Leu	
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118 <212> TYPE: PRT	
119 <213> ORGANISM: Human immunodeficiency virus	
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128 20 25 30	
131 Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu Gly Ala	
132 35 40 45	
135 Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln	
136 50 55 60	

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139 Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala Ala Glu  
 140 65 70 75 80  
 143 Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln  
 144 85 90 95  
 147 Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu  
 148 100 105 110  
 151 Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly  
 152 115 120 125  
 155 Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg  
 156 130 135 140  
 159 Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu  
 160 145 150 155 160  
 163 Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg Ala Glu  
 164 165 170 175  
 167 Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu Leu Val  
 168 180 185 190  
 171 Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu Gly Pro  
 172 195 200 205  
 175 Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly  
 176 210 215 220  
 179 Pro Lys Asn Gln Gln Leu Leu Ser Leu Trp Gly Cys Lys Gly Lys Leu  
 180 225 230 235 240  
 183 Val Cys Tyr Thr Ser Val Lys Trp Asn Gly Pro Gly His Lys Ala Arg  
 184 245 250 255  
 187 Val Leu  
 191 <210> SEQ ID NO: 3  
 192 <211> LENGTH: 795  
 193 <212> TYPE: DNA  
 194 <213> ORGANISM: Human immunodeficiency virus  
 197 <220> FEATURE:  
 198 <221> NAME/KEY: CDS -  
 199 <222> LOCATION: (16)..(789)  
 201 <400> SEQUENCE: 3  
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 203 Met Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val  
 204 1 5 10  
 206 cat cag gcc ata tca cct aga act tta aat gca tgg gta aaa gta gta 99  
 207 His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val  
 208 15 20 25  
 210 gaa gag aag gct ttc agc cca gaa gtg ata ccc atg ttt tca gca tta 147  
 211 Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu  
 212 30 35 40  
 214 tca gaa gga gcc acc cca caa gat tta aac acc atg cta aac aca gtg 195  
 215 Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val  
 216 45 50 55 60  
 218 ggg gga cat caa gca gcc atg caa atg tta aaa gag acc atc aat gag 243  
 219 Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu  
 220 65 70 75  
 222 gaa gct gca gaa tgg gat aga gtg cat cca gtg cat gca ggg cct att 291

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226	gca	cca	ggc	cag	atg	aga	gaa	cca	agg	gga	agt	gac	ata	gca	gga	act	339
227	Ala	Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	
228	95							100					105				
230	act	agt	acc	ctt	cag	gaa	caa	ata	gga	tgg	atg	aca	aat	aat	cca	cct	387
231	Thr	Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	
232	110							115				120					
234	atc	cca	gta	gga	gaa	att	tat	aaa	aga	tgg	ata	atc	ctg	gga	tta	aat	435
235	Ile	Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	
236	125							130				135				140	
238	aaa	ata	gta	aga	atg	tat	agc	cct	acc	agc	att	ctg	gac	ata	aga	caa	483
239	Lys	Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	
240								145				150				155	
242	gga	cca	aag	gaa	ccc	ttt	aga	gac	tat	gta	gac	cg	ttc	tat	aaa	act	531
243	Gly	Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	
244	160							165				170					
246	cta	aga	gcc	gag	caa	gct	tca	cag	gag	gta	aaa	aat	tgg	atg	aca	gaa	579
247	Leu	Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	
248	175							180				185					
250	acc	ttg	ttg	gtc	caa	aat	gcg	aac	cca	gat	tgt	aag	act	att	tta	aaa	627
251	Thr	Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	
252	190							195				200					
254	gca	ttg	gga	cca	gcg	gct	aca	cta	gaa	atg	atg	aca	gca	tgt	cag	675	
255	Ala	Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Met	Met	Thr	Ala	Cys	Gln		
256	205							210				215				220	
258	gga	gta	gga	gga	ccc	aaa	aat	caa	caa	aga	tta	aat	tta	tgg	ggg	tgt	723
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260								225				230				235	
262	aaa	ggg	aaa	ctt	att	tgt	tat	act	tcc	gtt	aaa	tgg	aat	gga	ccc	ggc	771
263	Lys	Gly	Lys	Leu	Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	
264	240							245				250					
266	cat	aag	gca	aga	gtt	ttg	taataa									795	
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273	<212>	TYPE:	PRT														
274	<213>	ORGANISM:	Human immunodeficiency virus														
276	<400>	SEQUENCE:	4														
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283								20				25				30	
286	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	Glu	Gly	Ala	
287								35				40				45	
290	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	Gly	His	Gln	
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294	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	Ala	Ala	Glu	

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302	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	Ser	Thr	Leu
303					100				105						110	
306	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile	Pro	Val	Gly
307					115				120						125	
310	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	Ile	Val	Arg
311					130				135						140	
314	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	Pro	Lys	Glu
315		145				150					155				160	
318	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	Arg	Ala	Glu
319						165				170					175	
322	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	Leu	Leu	Val
323					180					185					190	
326	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	Leu	Gly	Pro
327					195				200						205	
330	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	Val	Gly	Gly
331					210				215						220	
334	Pro	Lys	Asn	Gln	Gln	Arg	Leu	Asn	Leu	Trp	Gly	Cys	Lys	Gly	Lys	Leu
335		225				230					235				240	
338	Ile	Cys	Tyr	Thr	Ser	Val	Lys	Trp	Asn	Gly	Pro	Gly	His	Lys	Ala	Arg
339						245				250					255	
342	Val	Leu														
346	<210>	SEQ	ID	NO:	5											
347	<211>	LENGTH:	795													
348	<212>	TYPE:	DNA													
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352	<220>	FEATURE:														
353	<221>	NAME/KEY:	CDS													
354	<222>	LOCATION:	(16)..(789)													
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359					1				5					10		
361	cat	cag	gcc	ata	tca	cct	aga	act	tta	aat	gca	tgg	gta	aaa	gta	gta
362	His	Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val
363					15				20					25		
365	gaa	gag	aag	gct	ttc	agc	cca	gaa	gtg	ata	ccc	atg	ttt	tca	gca	tta
366	Glu	Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu
367					30				35					40		
369	tca	gaa	gga	gcc	acc	cca	caa	gat	tta	aac	acc	atg	cta	aac	aca	gtg
370	Ser	Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val
371					45				50			55		60		
373	ggg	gga	cat	caa	gca	gcc	atg	caa	atg	tta	aaa	gag	acc	atc	aat	gag
374	Gly	Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu
375							65			70				75		
377	gaa	gct	gca	gaa	tgg	gat	aga	gtg	cat	cca	gtg	cat	gca	ggg	cct	att
378	Glu	Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile

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Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:68,69,70,71,72,74,75,76

**VERIFICATION SUMMARY**

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